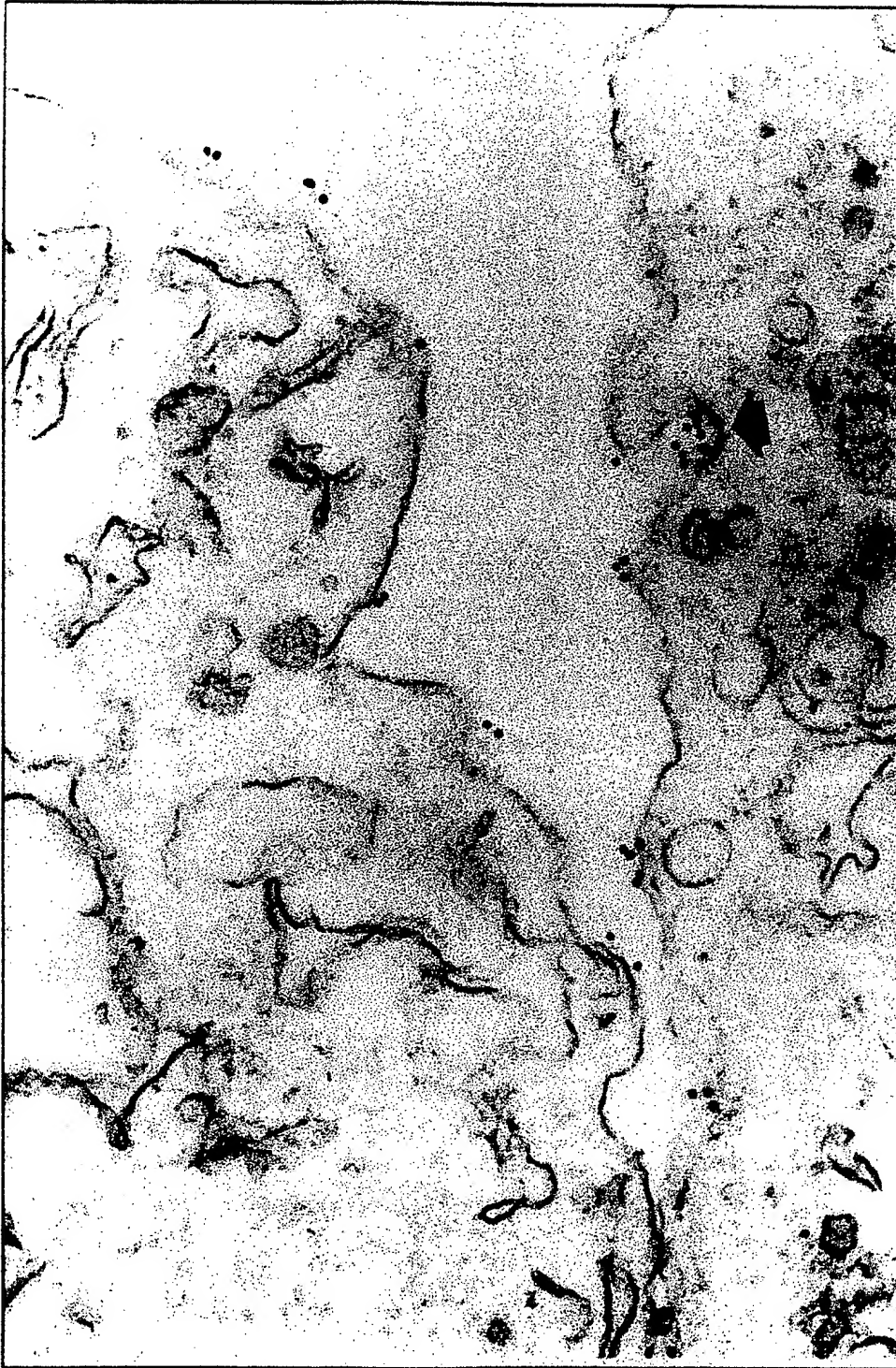


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**FIG. 1**

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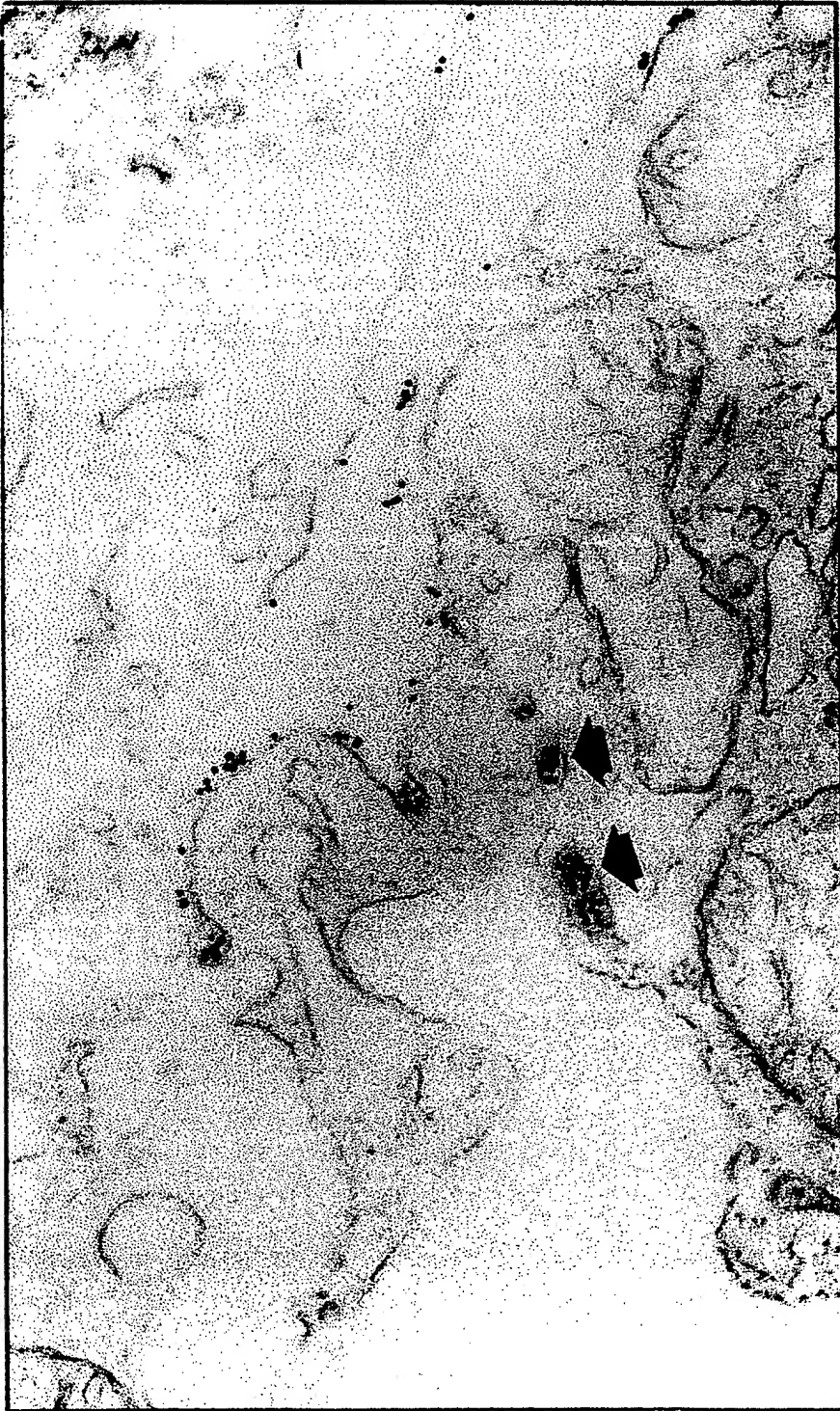
**FIG. 2**

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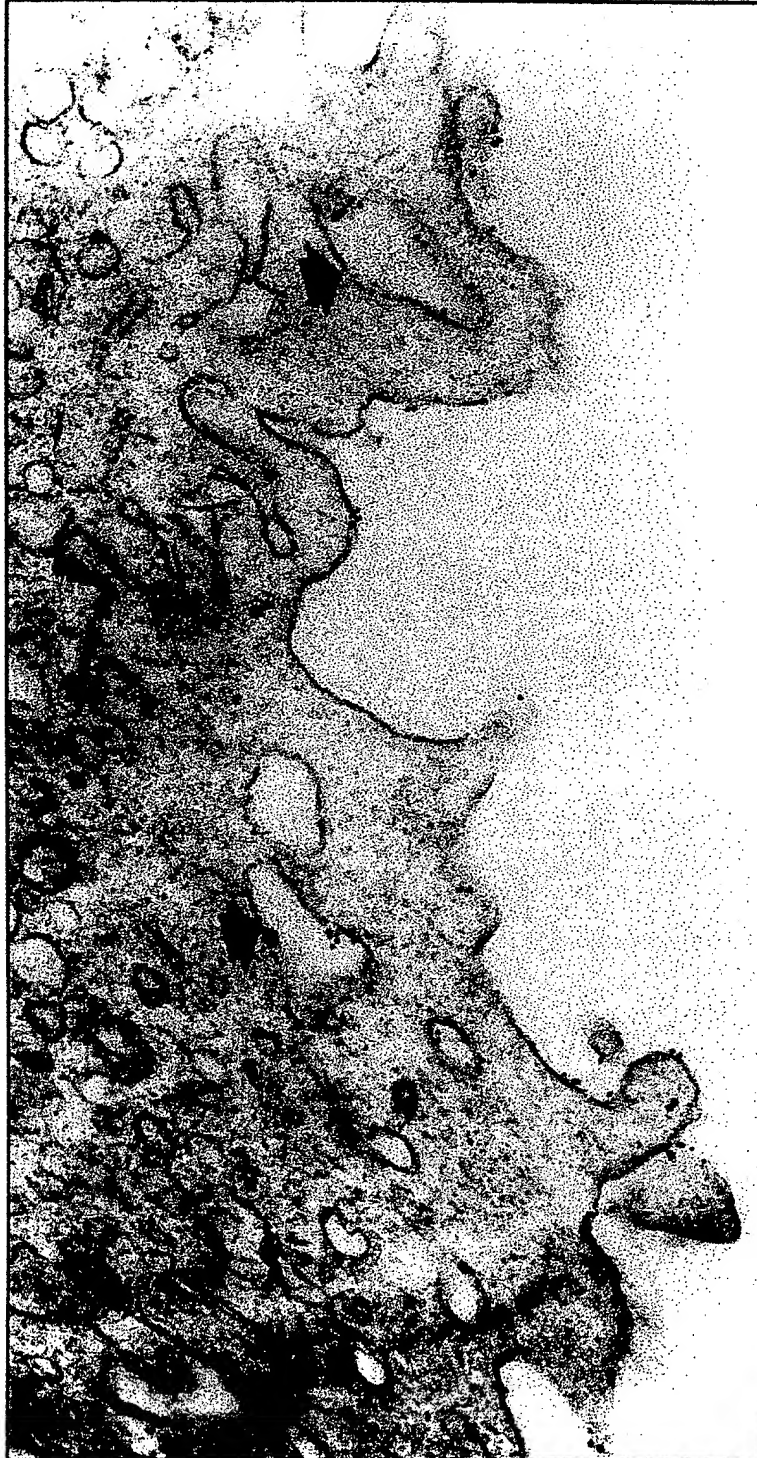
**FIG. 3**

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**FIG. 4**

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**FIG. 5**

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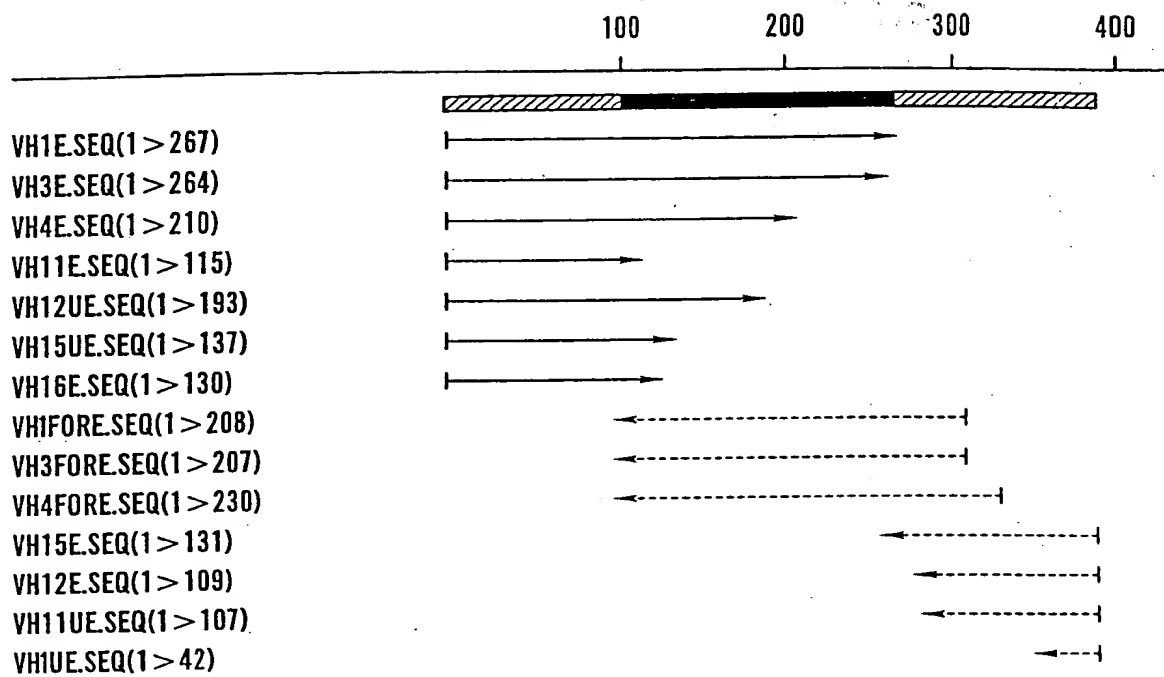


FIG. 6



**SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE**



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LIPMAN-PEARSON PROTEIN ALIGNMENT  
 KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115) J591VH.PRO	SEQ2(1>125) MUVHIIA.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>115)	(1>125)	75.6	2	10	125

```

      10      20      30      40      50
      ↓      ↓      ↓      ↓      ↓
EVQLQQSGPELVKPGTSVRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGGIT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFIDYYMNNWVKQSPGKSLEWIGDINFGNGGTS
      ↑      ↑      ↑      ↑      ↑      60
      10      20      30      40      50
      ↓      ↓      ↓      ↓      ↓
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWQGQGIT
YNQKF.:KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWQGQGIT
YNQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGIT
      ↑      ↑      ↑      ↑      ↑      120
      70      80      90      100     110

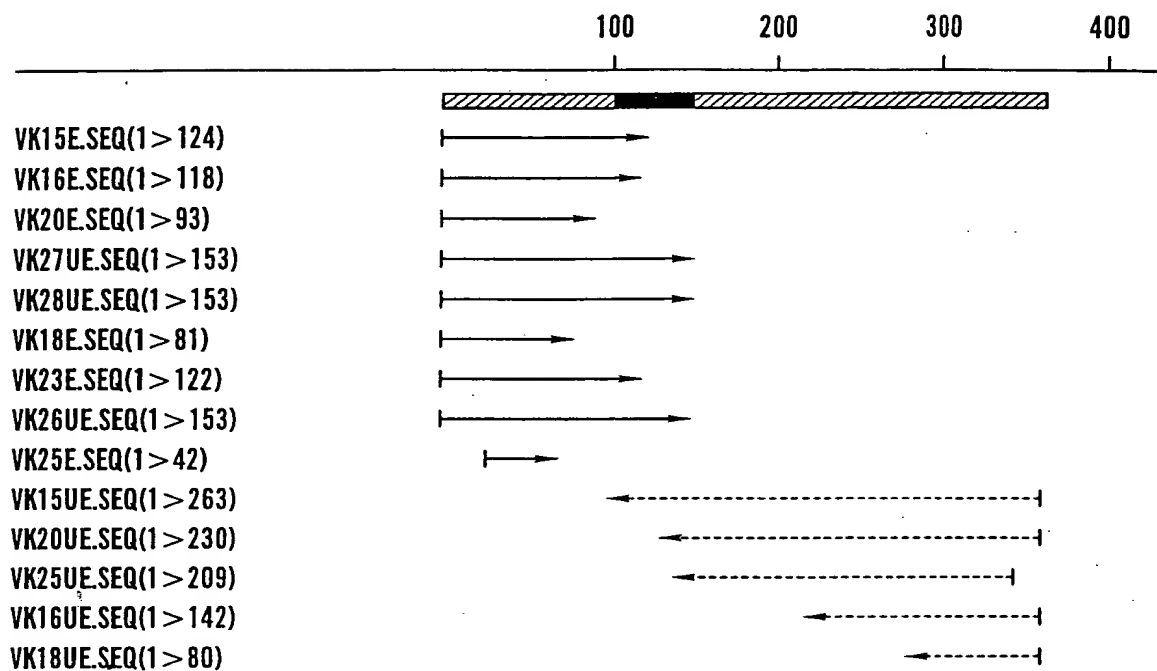
```

LTVSS  
 :TVSS  
 VIVSS

FIG. 8



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**FIG. 9**

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ENZYMES: ALL 74 ENZYMES (NO FILTER):  
 SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

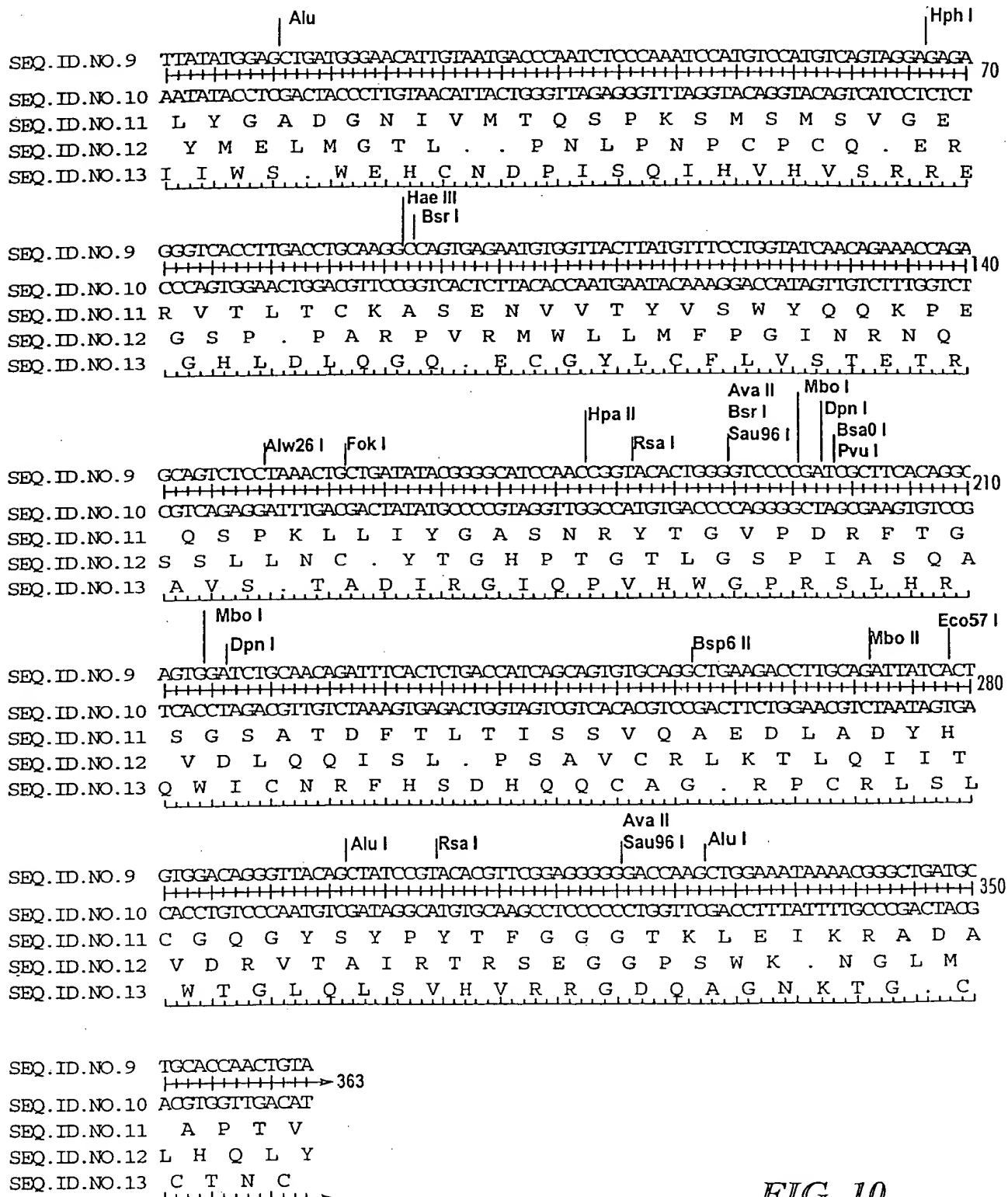


FIG. 10

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## LIPMAN-PEARSON PROTEIN ALIGNMENT

KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107)	SEQ2(1 > 1 1 1)	SIMILARITY	GAP	GAP	CONSENSUS
J591VK.PRO	MUVKV.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>107)	(1>109)	60.4	2	2	109

↓10      ↓20      ↓30      ↓40      ↓50  
NIVMTQSPKSMMSVGERVILTCKAS-ENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVP  
:I MIQSP.S:S S:G:RVT:TC:AS ::: .Y::WYQQKP. SPKLLIY AS. .:GVP  
DIQMTQSPSSLSASLGDRVITTCRASQDDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP  
↑10      ↑20      ↑30      ↑40      ↑50      ↑60  
↓60      ↓70      ↓80      ↓90      ↓100  
DRFTGSGSATDFTLTISVQAEDLADYHCGQGYSY-PYTFGGGKLEIK  
.RF:GSGS:TD::LTIS:::ED:A.Y C QG : P TFGGGKLEIK  
SRFSGSGSGIDYSLTISNLEQEDIATYFCQQGNTLPPTTFGGGKLEIK  
↑70      ↑80      ↑90      ↑100

FIG. 11